Jason J. Evans

Bioinformatics Engineering and Data Science

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Highlights



- Established and managed a highly-effective clinical bioinformatics group developing and supporting diverse systems with diverse data
- Wide breadth of experience both contributing and leading development of extensible, scalable software integrating big data with varied, complex data sets
- Deep expertise dedicated to bioinformatics research and engineering towards analysis, assay development, validation and clinical operations for diagnostic genetic testing
- Designed and implemented containerized cloud pipelines and supporting systems integrated into full end-to-end workflows
- Effective in the analysis and visualization of data. I have significant ability to manage, transform, and distill data sets
- I communicate in a way that makes technical concepts digestable to a variety of audiences

Education

University of Wisconsin-Madison

Bachelors of Science, Botany

Madison, WI

1999

Medical College of Wisconsin and Marquette University

Masters of Science, Joint Program in Bioinformatics

Milwaukee, WI

2009

Experience

Quest Diagnostics

Marlborough, MA

Sr. Staff Scientist/Sr. Manager, Bioinformatics

1/2018-Current

- Established and managed a highly skilled, high-functioning clinical bioinformatics group in development and in support of geneticists, variant scientists and lab operations as part of a highly-regulated genetic testing laboratory
- Led and contributed to extensible, scalable software integrating core analyses with all systems required in our end-to-end sample processing workflow
- Dedicated research and engineering towards primary analysis, assay development, validation and clinical operations

Projects developed from initial research through implementation, validation, and in clinical operations:

- Built first-in-kind long-read sequencing assay for quantification of tandem repeats using a CRISPR/Cas9 no-amp
- Extensive development of containerized, cloud-based high-throughput analysis pipelines and integrating systems for large scale, consumer-based assay processing 100,000 samples over a vear
- Performed key analyses contributing to actionable insights and algorithms applied to complex data sets in support of multiple labs with varied workflows
- · Led development for high volume cloud-based systems and the tools to register and find data, track provenance, and ease troubleshooting of cloud pipelines and supporting systems
- Drove extensible implementation of group's Python libraries to standardize logging, tracking, and connection between LIMS, cloud-based systems and interpretation and reporting databases
- Fostered extensibility and simplicity in all of the systems used in our production clinical setting

Courtagen Life Sciences

Woburn, MA

Clinical Bioinformatics Scientist, Annotation & Interpretation

11/2015-7/2017

- Supported and implemented of interpretation and reporting full stack web applications providing feature improvements and Lifecycle Management in a CAP/CLIA genetic testing environment
- Built web interfaces and backends to identify and queue confirmatory analysis for diagnostic purposes

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Experience (con'd)

Clinical Bioinformatician

Laboratory of Molecular Medicine/Partners Personalized Medicine

Cambridge, MA

9/2012-11/2015

- Produced end-to-end pipeline for distributed computation and variant calling for Whole Genome Sequencing in a CAP/CLIA genetic testing laboratory setting
- Implemented software to interface variant databases, variant annotation, and interpretation interfaces into a single, simple set of tools and resources

Harvard School of Public Health, Bioinformatics Core

Boston, MA 7/2011-8/2012

Bioinformatician

- Provided bioinformatics analyses and reports in support of contracting labs throughout HSPS
- Extensive contribution of tools and workflows towards the HSPS fork of the Galaxy Project

Marquette University, School of Biology

Milwaukee, WI

5/2007-1/2008

5/2001-5/2005

Research Associate, Molecular Biology

• Built molecular biology constructs for RNA Interference in *Chlamydomonas*

Applied Biosystems

Foster City, CA

Bioinformatics Scientist, Research & Development

- Built the computational analysis and system to run it in support of SNPlex custom oligo array
- Assisted in development of the first ABI 7900 high-throughput qPCR platform. Provided continued improvements in basecalling for the ABI 3700 sequencing instrument
- Leveraged the Celera human genome draft to identify putative drug targets in collaboration with contracted pharmaceutical companies

Celera Genomics Foster City, CA Scientist5/2000-5/2001

- Wet lab identification of full-length cDNA clones targeting putative drug targets
- cDNA library archival in a high-throughput cloning laboratory focused on isolating drug targets identified by draft genome

Publications

Tsai, E.A.; Shakbatyan, R.; Evans, J.; Rossetti, P.; Graham, C.; Sharma, H.; Lin, C.-F.; Lebo, M.S. Bioinformatics Workflow for Clinical Whole Genome Sequencing at Partners HealthCare Personalized Medicine. J. Pers. Med. 2016, 6, 12.

Technical Skills

Sequencing: PacBio Long-read, NGS Whole Exome, Whole

Genome

Stats & Data Science: R. Bioconductor ggplot2/dplyr/tidyverse, Pandas, Plotly Machine Learning: scikit-learn, PyTorch

Languages: Python, Ruby, Java, Javascript, CSS, SQL AWS: S3, API Gateway, IAM, ECR, Lambda, EC2, Batch

Containerization: Docker, Rancher

Variant Calling: Small, Copy Number, Structural, Tandem

repeat variation

Databases: Relational, NoSQL, Document

Regulatory: College of American Pathology (CAP), CLIA

Environments: Conda, Jupyter

Web Frameworks: Flask, FastAPI, VueJS

